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PUBLICATION NUMBER : 2001037489
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APPLICANT : MITSUBISHI CHEMICALS CORP;

INVENTOR : HATAKEYAMA KAZUHISA;

INT.CL. : C12N 15/09 C12M 1/00 C12Q 1/68 // C07K 14/195

TITLE : METHOD OF ANALYZING GENE

ABSTRACT : PROBLEM TO BE SOLVED: To provide a method of analyzing a gene by improving the analysis rate by means of immobilizing either a probe nucleic acid or a sample nucleic acid containing a target sequence complementary to the sequence of this probe nucleic acid on a base plate and reacting these nucleic acids in the presence of a double strand DNA-binding protein.

SOLUTION: On the gene analysis containing the detection of hybridization between a probe nucleic acid and a sample nucleic acid containing a target sequence complementary to the sequence of this probe nucleic acid, either the above probe nucleic acid or the sample nucleic acid is immobilized on a base plate and at least one of the above these nucleic acids is DNA. By forming the above hybridization in the presence of a double strand DNA-binding protein, e.g. Sulfolobus solfataricus-derived Sso7d protein or the like, the gene is analyzed rapidly with high sensitivity. This method can be utilized in the determination of the base sequence of nucleic acid, the gene diagnosis of infectious disease or hereditary disease, the expression monitoring of genomic gene, or the like.

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General Information

XP-002378912

Primary Accession # BD004299
Accession # BD004299
Entry Name EMBL:BD004299
Molecule Type unassigned DNA
Sequence Length 26
Entry Division SYN
Sequence Version BD004299.1
Creation Date 08-FEB-2002
Modification Date 08-FEB-2002

Description

Description Gene analysis method.
Keywords JP 2001037489-A/8;
Organism synthetic construct
Organism other sequences; artificial sequences.
Classification

References

1. Hatakeyama, K.;
Gene analysis method
Patent number JP2001037489-A/8, 13-FEB-2001. MITSUBISHI
CHEMICAL CORP.
Position 1-26

Features

Key	Location	Qualifier	Value
source	1..26		organism synthetic construct
			mol_type unassigned DNA
			db_xref taxon:32630

Sequence

Characteristics **Length: 26 BP, A Count:4, C Count:8, G Count:10, T Count:4, Other Count:0**

Sequence

>embl|BD004299|BD004299 Gene analysis method.
agtctcggagtcgggcatggccac

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